SEQUENCE LISTING

<110> Penttila, Merja E.
      Ward, Michael
      Wang, Huaming
      Valkonen, Mari J.
      Saloheimo, Markku

<120> Increased Production of Secreted
    Proteins by Recombinant Eukaryotic Cells

<130> GC590-2

<140> US 09/816,227
<141> 2001-03-23

<150> US 09/534,692
<151> 2000-03-24

<160> 63

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<212> DNA
<213> Trichoderma reesei

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aagaaacagt tggtccgacg tcacaagcac attcacaaaa atcaaacaac atatccccat    360
ctttcatata caccacacgc ttatgcagtg agagagcacg agagaagcat cgtcataatc    420
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cagcagtcgt ctccctcgt caagtttgag gcctctcccg ccgaatcctt cctctccgcc    540
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caaacgttac tgtagaaaac gtgcaaagac ggaagatgaa aaggagcagc gccgcgtcga    900
gcgtgttctc cgcaaccgcc gcgccgcgca gtcctcgcgc gagcgcaaga ggctcgaggt    960
cgaggctctc gagaagcgca acaaggagct cgagacgctc ctcatcaacg tccagaagac   1020
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tcccgcgtct ccactgattc gacacaacgt cctgcagaga tgttgtgcga cccgcagtgt   1440
caatcggtgg agatgccgct gtccctgtct tctcagacga cgccggcgca aactgccttg   1500
gcctggaccc tgttcatcag gatgatggtc ctttcagcat cggccattct ttcggcctgt   1560
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tcccctccga ctacgacttc gacatcaacg acttcctcac agacgacgca aaccacgccg      1740
cctatgacat tgtggcagcg agcaactatg ccgctgcgga ccgcgagctc gacctcgaga      1800
tccacgaccc tgagaatcag atcccttcgc gacattctat ccagcagccc cagtctggcg      1860
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cccgagaagc gcgcctcctt ggcagacaag aagaaccgac aacaacaaca acaacaacac      2160
cagtatcaga ttccttcgtt ttcaaaatag ttagcatatg tggtttttta atgggcaatg      2220
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<212> PRT
<213> Trichoderma reesei

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Ala Asp Ser Thr Pro Ser Thr Leu Asn Pro Arg Asp Met Met Thr Pro
        35                  40                  45
Asp Ser Val Ala Asp Ile Asp Ser Arg Leu Ser Val Ile Pro Glu Ser
    50                  55                  60
Gln Asp Ala Glu Asp Asp Glu Ser His Ser Thr Ser Ala Thr Ala Pro
65                  70                  75                  80
Ser Thr Ser Glu Lys Lys Pro Val Lys Lys Arg Lys Ser Trp Gly Gln
                85                  90                  95
Val Leu Pro Glu Pro Lys Thr Asn Leu Pro Pro Arg Lys Arg Ala Lys
            100                 105                 110
Thr Glu Asp Glu Lys Glu Gln Arg Arg Val Glu Arg Val Leu Arg Asn
            115                 120                 125
Arg Arg Ala Ala Gln Ser Ser Arg Glu Arg Lys Arg Leu Glu Val Glu
    130                 135                 140
Ala Leu Glu Lys Arg Asn Lys Glu Leu Glu Thr Leu Leu Ile Asn Val
145                 150                 155                 160
Gln Lys Thr Asn Leu Ile Leu Val Glu Glu Leu Asn Arg Phe Arg Arg
                165                 170                 175
Ser Ser Gly Val Val Thr Arg Ser Ser Ser Pro Leu Asp Ser Leu Gln
            180                 185                 190
Asp Ser Ile Thr Leu Ser Gln Gln Leu Phe Gly Ser Arg Asp Gly Gln
        195                 200                 205
Thr Met Ser Asn Pro Glu Gln Ser Leu Met Asp Gln Ile Met Arg Ser
    210                 215                 220
Ala Ala Asn Pro Thr Val Asn Pro Ala Ser Leu Ser Pro Ser Leu Pro
225                 230                 235                 240
Pro Ile Ser Asp Lys Glu Phe Gln Thr Lys Glu Glu Asp Glu Glu Gln
                245                 250                 255
Ala Asp Glu Asp Glu Glu Met Glu Gln Thr Trp His Glu Thr Lys Glu
            260                 265                 270
Ala Ala Ala Ala Lys Glu Lys Asn Ser Lys Gln Ser Arg Val Ser Thr
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2

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              275                    280                    285
Asp Ser Thr Gln Arg Pro Ala Val Ser Ile Gly Gly Asp Ala Ala Val
      290                    295                    300
Pro Val Phe Ser Asp Asp Ala Gly Ala Asn Cys Leu Gly Leu Asp Pro
305                    310                    315                    320
Val His Gln Asp Asp Gly Pro Phe Ser Ile Gly His Ser Phe Gly Leu
                  325                    330                    335
Ser Ala Ala Leu Asp Ala Asp Arg Tyr Leu Leu Glu Ser Gln Leu Leu
              340                    345                    350
Ala Ser Pro Asn Ala Ser Thr Val Asp Asp Asp Tyr Leu Ala Gly Asp
      355                    360                    365
Ser Ala Ala Cys Phe Thr Asn Pro Leu Pro Ser Asp Tyr Asp Phe Asp
      370                    375                    380
Ile Asn Asp Phe Leu Thr Asp Asp Ala Asn His Ala Ala Tyr Asp Ile
385                    390                    395                    400
Val Ala Ala Ser Asn Tyr Ala Ala Ala Asp Arg Glu Leu Asp Leu Glu
                  405                    410                    415
Ile His Asp Pro Glu Asn Gln Ile Pro Ser Arg His Ser Ile Gln Gln
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Pro Gln Ser Gly Ala Ser Ser His Gly Cys Asp Asp Gly Gly Ile Ala
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Val Gly Val
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<210> 3
<211> 1615
<212> DNA
<213> Aspergillus nidulans

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aactcccaac ttcgcaacct catcaaccac ctgcttccgt ctagttgcag ttatcagact       180
tgagttgtat gaaatcagca gaccggtttt cgccagtgaa aatggaggac gctttcgcaa       240
actctttgcc tactaccccg tcattggagg ttcctgtgct cactgtctcc ccggctgaca       300
catctcttcg gacgaagaat gtggtggctc agacaaagcc tgaggagaag aagccagcga       360
agaaaagaaa gtcctggggc caggaattac cagttcccaa gacaaactta cctccaaggt       420
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aagacagaag atgagaaaga gcagcgccgg attgagcgag ttcttcgcaa ccgcgcagcc       540
gcacaaacct ctcgcgagcg caagagactt gaaatggaga agttagaaag cgagaagatt       600
gatatggaac aacaaaacca gttccttctt cagcgtctcg cccagatgga ggctgagaac       660
aaccgtttaa gtcagcaagt tgctcagcta tccgcggagg ttcggggatc ccgccacagc       720
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caggaagggg atgaggttcc tctggaccgc atccttttc caactccctc cgtgaccgac       840
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tcgacggaag accgtctggt tcccgatgtt gtagagggtc gatggagctg ggaatccttg      1380
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<211> 349
<212> PRT
<213> Aspergillus nidulans

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            20   25   30
Ser Pro Ala Asp Thr Ser Leu Arg Thr Lys Asn Val Val Ala Gln Thr
            35   40   45
Lys Pro Glu Glu Lys Lys Pro Ala Lys Lys Arg Lys Ser Trp Gly Gln
    50   55   60
Glu Leu Pro Val Pro Lys Thr Asn Leu Pro Pro Arg Lys Arg Ala Lys
65   70   75   80
Thr Glu Asp Glu Lys Glu Gln Arg Arg Ile Glu Arg Val Leu Arg Asn
                85   90   95
Arg Ala Ala Ala Gln Thr Ser Arg Glu Arg Lys Arg Leu Glu Met Glu
            100   105   110
Lys Leu Glu Ser Glu Lys Ile Asp Met Glu Gln Gln Asn Gln Phe Leu
            115   120   125
Leu Gln Arg Leu Ala Gln Met Glu Ala Glu Asn Asn Arg Leu Ser Gln
            130   135   140
Gln Val Ala Gln Leu Ser Ala Glu Val Arg Gly Ser Arg His Ser Thr
145   150   155   160
Pro Thr Ser Ser Ser Pro Ala Ser Val Ser Pro Thr Leu Thr Pro Thr
                165   170   175
Leu Phe Lys Gln Glu Gly Asp Glu Val Pro Leu Asp Arg Ile Pro Phe
            180   185   190
Pro Thr Pro Ser Val Thr Asp Tyr Ser Pro Thr Leu Lys Pro Ser Ser
            195   200   205
Leu Ala Glu Ser Pro Asp Leu Thr Gln His Pro Ala Val Ser Val Gly
            210   215   220
Gly Leu Glu Gly Asp Glu Ser Ala Leu Thr Leu Phe Asp Leu Gly Ala
225   230   235   240
Ser Ile Lys His Glu Pro Thr His Asp Leu Thr Ala Pro Leu Ser Asp
                245   250   255
Asp Asp Phe Arg Arg Leu Phe Asn Gly Asp Ser Ser Leu Glu Ser Asp
            260   265   270
Ser Ser Leu Leu Glu Asp Gly Phe Ala Phe Asp Val Leu Asp Ser Gly
            275   280   285
Asp Leu Ser Ala Phe Pro Phe Asp Ser Met Val Asp Phe Asp Thr Glu
            290   295   300
Pro Val Thr Leu Glu Asp Leu Glu Gln Thr Asn Gly Leu Ser Asp Ser
305   310   315   320
Ala Ser Cys Lys Ala Ala Ser Leu Gln Pro Ser His Gly Ala Ser Thr
                325   330   335
Ser Arg Cys Asp Gly Gln Gly Ile Ala Ala Gly Ser Ala
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<210> 5
<211> 451
<212> PRT
<213> Trichoderma reesei

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<400> 5

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Ala Asp Ser Thr Pro Ser Thr Leu Asn Pro Arg Asp Met Met Thr Pro
                35                  40                  45
Asp Ser Val Ala Asp Ile Asp Ser Arg Leu Ser Val Ile Pro Glu Ser
    50                  55                  60
Gln Asp Ala Glu Asp Asp Glu Ser His Ser Thr Ser Ala Thr Ala Pro
65                  70                  75                  80
Ser Thr Ser Glu Lys Lys Pro Val Lys Lys Arg Lys Ser Trp Gly Gln
                85                  90                  95
Val Leu Pro Glu Pro Lys Thr Asn Leu Pro Pro Arg Lys Arg Ala Lys
                100                 105                 110
Thr Glu Asp Glu Lys Glu Gln Arg Arg Val Glu Arg Val Leu Arg Asn
                115                 120                 125
Arg Arg Ala Ala Gln Ser Ser Arg Glu Arg Lys Arg Leu Glu Val Glu
    130                 135                 140
Ala Leu Glu Lys Arg Asn Lys Glu Leu Glu Thr Leu Leu Ile Asn Val
145                 150                 155                 160
Gln Lys Thr Asn Leu Ile Leu Val Glu Glu Leu Asn Arg Phe Arg Arg
                165                 170                 175
Ser Ser Gly Val Val Thr Arg Ser Ser Ser Pro Leu Asp Ser Leu Gln
                180                 185                 190
Asp Ser Ile Thr Leu Ser Gln Gln Leu Phe Gly Ser Arg Asp Gly Gln
    195                 200                 205
Thr Met Ser Asn Pro Glu Gln Ser Leu Met Asp Gln Ile Met Arg Ser
    210                 215                 220
Ala Ala Asn Pro Thr Val Asn Pro Ala Ser Leu Ser Pro Ser Leu Pro
225                 230                 235                 240
Pro Ile Ser Asp Lys Glu Phe Gln Thr Lys Glu Glu Asp Glu Glu Gln
                245                 250                 255
Ala Asp Glu Asp Glu Glu Met Glu Gln Thr Trp His Glu Thr Lys Glu
                260                 265                 270
Ala Ala Ala Ala Lys Glu Lys Asn Ser Lys Gln Ser Arg Val Ser Thr
    275                 280                 285
Asp Ser Thr Gln Arg Pro Ala Val Ser Ile Gly Gly Asp Ala Ala Val
    290                 295                 300
Pro Val Phe Ser Asp Asp Ala Gly Ala Asn Cys Leu Gly Leu Asp Pro
305                 310                 315                 320
Val His Gln Asp Asp Gly Pro Phe Ser Ile Gly His Ser Phe Gly Leu
                325                 330                 335
Ser Ala Ala Leu Asp Ala Asp Arg Tyr Leu Leu Glu Ser Gln Leu Leu
                340                 345                 350
Ala Ser Pro Asn Ala Ser Thr Val Asp Asp Asp Tyr Leu Ala Gly Asp
                355                 360                 365
Ser Ala Ala Cys Phe Thr Asn Pro Leu Pro Ser Asp Tyr Asp Phe Asp
    370                 375                 380
Ile Asn Asp Phe Leu Thr Asp Asp Ala Asn His Ala Ala Tyr Asp Ile
385                 390                 395                 400
Val Ala Ala Ser Asn Tyr Ala Ala Ala Asp Arg Glu Leu Asp Leu Glu
                405                 410                 415
Ile His Asp Pro Glu Asn Gln Ile Pro Ser Arg His Ser Ile Gln Gln
                420                 425                 430
Pro Gln Ser Gly Ala Ser Ser His Gly Cys Asp Asp Gly Gly Ile Ala
                435                 440                 445
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5

Val Gly Val
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<212> PRT
<213> Aspergillus nidulans

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                20   25   30
Ser Pro Ala Asp Thr Ser Leu Arg Thr Lys Asn Val Val Ala Gln Thr
            35   40   45
Lys Pro Glu Glu Lys Lys Pro Ala Lys Lys Arg Lys Ser Trp Gly Gln
        50   55   60
Glu Leu Pro Val Pro Lys Thr Asn Leu Pro Pro Arg Lys Arg Ala Lys
65   70   75   80
Thr Glu Asp Glu Lys Glu Gln Arg Arg Ile Glu Arg Val Leu Arg Asn
                85   90   95
Arg Ala Ala Ala Gln Thr Ser Arg Glu Arg Lys Arg Leu Glu Met Glu
            100   105   110
Lys Leu Glu Ser Glu Lys Ile Asp Met Glu Gln Gln Asn Gln Phe Leu
        115   120   125
Leu Gln Arg Leu Ala Gln Met Glu Ala Glu Asn Asn Arg Leu Ser Gln
        130   135   140
Gln Val Ala Gln Leu Ser Ala Glu Val Arg Gly Ser Arg His Ser Thr
145   150   155   160
Pro Thr Ser Ser Ser Pro Ala Ser Val Ser Pro Thr Leu Thr Pro Thr
                165   170   175
Leu Phe Lys Gln Glu Gly Asp Glu Val Pro Leu Asp Arg Ile Pro Phe
                180   185   190
Pro Thr Pro Ser Val Thr Asp Tyr Ser Pro Thr Leu Lys Pro Ser Ser
            195   200   205
Leu Ala Glu Ser Pro Asp Leu Thr Gln His Pro Ala Val Ser Val Gly
        210   215   220
Gly Leu Glu Gly Asp Glu Ser Ala Leu Thr Leu Phe Asp Leu Gly Ala
225   230   235   240
Ser Ile Lys His Glu Pro Thr His Asp Leu Thr Ala Pro Leu Ser Asp
                245   250   255
Asp Asp Phe Arg Arg Leu Phe Asn Gly Asp Ser Ser Leu Glu Ser Asp
                260   265   270
Ser Ser Leu Leu Glu Asp Gly Phe Ala Phe Asp Val Leu Asp Ser Gly
            275   280   285
Asp Leu Ser Ala Phe Pro Phe Asp Ser Met Val Asp Phe Asp Thr Glu
        290   295   300
Pro Val Thr Leu Glu Asp Leu Glu Gln Thr Asn Gly Leu Ser Asp Ser
305   310   315   320
Ala Ser Cys Lys Ala Ala Ser Leu Gln Pro Ser His Gly Ala Ser Thr
                325   330   335
Ser Arg Cys Asp Gly Gln Gly Ile Ala Ala Gly Ser Ala
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<211> 1265
<212> DNA

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cacaatctga tatactacag gaatctggga ttgccagtct tcccaagccg tggtcgaatt     180
cgttcgccgc ggtatcgcgg ccaagcagga tctctatcgg atttgtgaaa acatgatgga     240
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ggttgctaac ggcgacggcc cttgtgctcc gcccgaatac ggcaagtctc tcgaggaacc     420
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ccttctatct cttgttttaa tcccatcttc ttactttta cgagctcatc cagatcaaat    1080
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<210> 8
<211> 130
<212> PRT
<213> Aspergillus nidulans
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            20                  25                  30
Trp Asp Cys Gln Ser Ser Gln Ala Val Val Glu Phe Val Arg Arg Gly
        35                  40                  45
Ile Ala Ala Lys Gln Asp Leu Tyr Arg Ile Cys Glu Asn Met Met Asp
    50                  55                  60
Asn Cys Leu Ala Ser Asn Ser Glu Thr Gly Gly Val Gly Cys Asp Asn
65                  70                  75                  80
Met Thr Met Val Ile Ile Gly Leu Leu Asn Gly Lys Thr Lys Glu Glu
                85                  90                  95
Trp Tyr Asn Gln Ile Ala Glu Arg Val Ala Asn Gly Asp Gly Pro Cys
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Ala Pro Pro Glu Tyr Gly Lys Ser Leu Glu Glu Pro Thr Ala Ser Asn
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Pro Tyr
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<210> 9
<211> 1824
<212> DNA
<213> Trichoderma reesei
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<400> 9.

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cctgagtacc aaacgataga aacaagactg ctatctttgt cgtgctgcct cctcccctcc     180
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aatatgccga gttccgcggt cccggcgttc accacaacta cgaagacagc gacagcggct    1260
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tcgttaaaaa aaaaaaaaaa aaaa                                           1824
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<210> 10
<211> 438
<212> PRT
<213> Trichoderma reesei

<400> 10
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Met Gly Gln Thr Leu Ser Glu Pro Val Val Glu Lys Thr Ser Glu Lys
1               5                   10                  15
Gly Glu Asp Asp Arg Leu Ile Tyr Gly Val Ser Ala Met Gln Gly Trp
            20                  25                  30
Arg Ile Ser Met Glu Asp Ala His Thr Ala Glu Leu Asn Leu Pro Pro
        35                  40                  45
Pro Asp Asn Asp Thr Lys Thr His Pro Asp Arg Leu Ser Phe Phe Gly
    50                  55                  60
Val Phe Asp Gly His Gly Gly Asp Lys Val Ala Leu Phe Ala Gly Glu
65                  70                  75                  80
Asn Ile His Asn Ile Val Phe Lys Gln Glu Ser Phe Lys Ser Gly Asp
                85                  90                  95
Tyr Ala Gln Gly Leu Lys Asp Gly Phe Leu Ala Thr Asp Arg Ala Ile
                100                 105                 110
Leu Asn Asp Pro Lys Tyr Glu Glu Glu Val Ser Gly Cys Thr Ala Cys
            115                 120                 125
Val Thr Leu Ile Ala Gly Asn Lys Leu Tyr Val Ala Asn Ala Gly Asp
        130                 135                 140
Ser Arg Ser Val Leu Gly Ile Lys Gly Arg Ala Lys Pro Leu Ser Asn
```

```
145                    150                    155                    160
Asp His Lys Pro Gln Leu Glu Thr Glu Lys Asn Arg Ile Thr Ala Ala
                 165                    170                    175
Gly Gly Phe Val Asp Phe Gly Arg Val Asn Gly Asn Leu Ala Leu Ser
                 180                    185                    190
Arg Ala Ile Gly Asp Phe Glu Phe Lys Lys Ser Ala Glu Leu Ser Pro
             195                    200                    205
Glu Asn Gln Ile Val Thr Ala Phe Pro Asp Val Glu Val His Glu Leu
         210                    215                    220
Thr Glu Glu Asp Glu Phe Leu Val Ile Ala Cys Asp Gly Ile Trp Asp
225                    230                    235                    240
Cys Gln Ser Ser Gln Ala Val Val Glu Phe Val Arg Arg Gly Ile Ala
                 245                    250                    255
Ala Lys Gln Asp Leu Asp Lys Ile Cys Glu Asn Met Met Asp Asn Cys
             260                    265                    270
Leu Ala Ser Asn Ser Glu Thr Gly Gly Val Gly Cys Asp Asn Met Thr
         275                    280                    285
Met Val Ile Ile Gly Phe Leu His Gly Lys Thr Lys Glu Glu Trp Tyr
     290                    295                    300
Asp Glu Ile Ala Lys Arg Val Ala Asn Gly Asp Gly Pro Cys Ala Pro
305                    310                    315                    320
Pro Glu Tyr Ala Glu Phe Arg Gly Pro Gly Val His His Asn Tyr Glu
                 325                    330                    335
Asp Ser Asp Ser Gly Tyr Asp Val Asp Ala Asp Ser Gly Gly Lys Phe
             340                    345                    350
Ser Leu Ala Gly Ser Arg Gly Arg Ile Ile Phe Leu Gly Asp Gly Thr
             355                    360                    365
Glu Val Leu Thr Gly Ser Asp Asp Thr Glu Met Phe Asp Asn Ala Asp
         370                    375                    380
Glu Asp Lys Asp Leu Ala Ser Gln Val Pro Lys Ser Ser Gly Lys Thr
385                    390                    395                    400
Asp Ala Lys Glu Glu Thr Glu Ala Lys Pro Ala Pro Glu Ala Glu Ser
                 405                    410                    415
Ser Lys Pro Ala Asp Gly Ser Glu Lys Lys Gln Asp Glu Lys Thr Pro
             420                    425                    430
Glu Glu Ser Lys Lys Asp
             435
```

<210> 11
<211> 1570
<212> DNA
<213> Aspergillus nidulans

<400> 11

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cggaggcaag agtcatagac gcgggaagaa gaaaattgag agtgagaaag aggaatctga    60
tcacgcccct ggcaccttgc aaccccggc tgggcccgat gccgggttag ctctcacccg    120
cactgcatct aatgaggtgt ttgaagcgga cggtgtcatc cagattggcc gtttgaaggt    180
ctttacggct gacgttctgg gtcatggaag ccacgggaca gttgtttacc gcgggtcgtt    240
tgacggccga gacgtcgcgg tcaaacgtat gctggtggag ttctatgata ttgcatcgca    300
cgaagtggga ttgttgcagg aaagcgatga tcataacaac gttatccgat gttattgccg    360
tgagcaagcc aagggtttct tctacatcgc ccttgaactg tgtccggctt ctttgcagga    420
tgtggtagaa cgaccagacg cgttcccgca gctagtcaat ggtggcttgg atatgccgga    480
cgtcttgcgt caaattgtcg ccggtgtccg gtacctacac tctctcaaaa tcgtacaccg    540
tgacttgaag cctcaaaata tcctggtcgc cgctcctcga ggccgtatcg gttctcgggc    600
catccggctt ctgatttcgg actttggctt gtgcaagaaa cttgaggata ccagagttc    660
attcagggca accacggccc atgctgctgg tactccgggt ggagggctcc cgaactgctt    720
gtggatgacg acaagagccg gtaatcaggg ttcagagtct caaaatacgg agtcatctga    780
```

9

```
gccggcggtc gtcgatcccc agacgaatcg acgagccacc cgagccattg atatcttctc      840
cctgggatgt gtcttctact acgtcctaac tcgaggatgt catccttttg acaagaatgg      900
caagttcatg cgcgaagcaa atatcgtcaa ggggaatttc aatctcgatg agttacagcg      960
tctaggagag tatgcgtttg aagcagacga tcttatccga tcaatgttgg cacttgatcc     1020
acgtcaacgg tatgtcccaa caacatcttc ctttgccttg tggcgtagcg tactaatctc     1080
cacagccccg acgcaagcgc tgtgttaacc catcctttct tctggaatcc gtccgaccgc     1140
cttagcttcc tctgtgacgt tcggaccac ttcgagttcg aaccgagaga tcctccatct     1200
gacgctcttc tgtgtctaga gtctgtagcc tctgatgtca ttggccctga aatgaatcct     1260
caaactcctg ccaaaggact tcaaagacag tctcggaagc agcgaaaata caccggctcc     1320
aaaatgctgg acttgatgcg agccctgcgg aacaagcgca accactacaa tgatatgccg     1380
gagcatttga aagctcatat tggtgggctg ccggagggtt acttgaattt ctggaccgtg     1440
cgtttcccga gtttgctgat gagttgtcat tgggtgattg ttgaactggg attgacgaag     1500
acggatcggt ccaagagat attttacgcc attggagtag gttgttgcgt actggttcag     1560
aaatatattg                                                            1570
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<210> 12
<211> 504
<212> PRT
<213> Aspergillus nidulans

<400> 12

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Gly Gly Lys Ser His Arg Arg Gly Lys Lys Lys Ile Glu Ser Glu Lys
 1               5                  10                  15
Glu Glu Ser Asp His Ala Pro Gly Thr Leu Gln Pro Pro Ala Gly Pro
            20                  25                  30
Asp Ala Gly Leu Ala Leu Thr Arg Thr Ala Ser Asn Glu Val Phe Glu
        35                  40                  45
Ala Asp Gly Val Ile Gln Ile Gly Arg Leu Lys Val Phe Thr Ala Asp
    50                  55                  60
Val Leu Gly His Gly Ser His Gly Thr Val Val Tyr Arg Gly Ser Phe
65                  70                  75                  80
Asp Gly Arg Asp Val Ala Val Lys Arg Met Leu Val Glu Phe Tyr Asp
                85                  90                  95
Ile Ala Ser His Glu Val Gly Leu Leu Gln Glu Ser Asp Asp His Asn
            100                 105                 110
Asn Val Ile Arg Cys Tyr Cys Arg Glu Gln Ala Lys Gly Phe Phe Tyr
            115                 120                 125
Ile Ala Leu Glu Leu Cys Pro Ala Ser Leu Gln Asp Val Val Glu Arg
    130                 135                 140
Pro Asp Ala Phe Pro Gln Leu Val Asn Gly Gly Leu Asp Met Pro Asp
145                 150                 155                 160
Val Leu Arg Gln Ile Val Ala Gly Val Arg Tyr Leu His Ser Leu Lys
                165                 170                 175
Ile Val His Arg Asp Leu Lys Pro Gln Asn Ile Leu Val Ala Ala Pro
            180                 185                 190
Arg Gly Arg Ile Gly Ser Arg Ala Ile Arg Leu Leu Ile Ser Asp Phe
        195                 200                 205
Gly Leu Cys Lys Lys Leu Glu Asp Asn Gln Ser Ser Phe Arg Ala Thr
    210                 215                 220
Thr Ala His Ala Ala Gly Thr Pro Gly Gly Gly Leu Pro Asn Cys Leu
225                 230                 235                 240
Trp Met Thr Thr Arg Ala Gly Asn Gln Gly Ser Glu Ser Gln Asn Thr
                245                 250                 255
Glu Ser Ser Glu Pro Ala Val Val Asp Pro Gln Thr Asn Arg Arg Ala
            260                 265                 270
Thr Arg Ala Ile Asp Ile Phe Ser Leu Gly Cys Val Phe Tyr Tyr Val
        275                 280                 285
```

10

```
Leu Thr Arg Gly Cys His Pro Phe Asp Lys Asn Gly Lys Phe Met Arg
    290                     295                 300
Glu Ala Asn Ile Val Lys Gly Asn Phe Asn Leu Asp Glu Leu Gln Arg
305                     310                 315                 320
Leu Gly Glu Tyr Ala Phe Glu Ala Asp Asp Leu Ile Arg Ser Met Leu
                325                 330                 335
Ala Leu Asp Pro Arg Gln Arg Pro Asp Ala Ser Ala Val Leu Thr His
            340                 345                 350
Pro Phe Phe Trp Asn Pro Ser Asp Arg Leu Ser Phe Leu Cys Asp Val
            355                 360                 365
Ser Asp His Phe Glu Phe Glu Pro Arg Asp Pro Pro Ser Asp Ala Leu
    370                 375                 380
Leu Cys Leu Glu Ser Val Ala Ser Asp Val Ile Gly Pro Glu Met Asn
385                 390                 395                 400
Pro Gln Thr Pro Ala Lys Gly Leu Gln Arg Gln Ser Arg Lys Gln Arg
                405                 410                 415
Lys Tyr Thr Gly Ser Lys Met Leu Asp Leu Met Arg Ala Leu Arg Asn
            420                 425                 430
Lys Arg Asn His Tyr Asn Asp Met Pro Glu His Leu Lys Ala His Ile
            435                 440                 445
Gly Gly Leu Pro Glu Gly Tyr Leu Asn Phe Trp Thr Val Arg Phe Pro
    450                 455                 460
Ser Leu Leu Met Ser Cys His Trp Val Ile Val Glu Leu Gly Leu Thr
465                 470                 475                 480
Lys Thr Asp Arg Phe Gln Glu Ile Phe Tyr Ala Ile Gly Val Gly Cys
                485                 490                 495
Cys Val Leu Val Gln Lys Tyr Ile
                500

<210> 13
<211> 4528
<212> DNA
<213> Trichoderma reesei

<400> 13
gcacgagcaa gatacggcct ctcgcaccaa ggagacacgc atattcgtgg taccatcggc      60
tgagggtgaa ggggggttca acacagcaca actcagcgac cactggactg gtggagccga     120
agcccacgat cgaatccaca gcctgcacca ctttctcctc gtcatattcg cggggactca     180
caagcggttt ccgttgcctt cgaattcgac agagctgcga ctgcgagtca tttcagcgac     240
tctaaaccta ctcctttggc tgctgcgcgg gactggttct gcccagcctc tcctactcga     300
ccaaccgacg tcctcttttct gcttcctcat cccttctcc tttgacgtcc gagcgtcaga     360
gcgaattttt ccttgcttct tcgtttgggc cgggaatggc ttctctggca tcgcaacagc     420
ctctacctct ccgttggtag agccatagcc tgcagctccc catgtgatcc gctctccgtc     480
tctccggcac cccgactttc gtctcgatca tgatgcggcg acccccgagc caaggacgat     540
ggtccgcgtc gcatcagaag ctctcctggc ttttgccttt attctcatac catggctcca     600
acttgccgat gctcagcagc agcctcagca gccccagatt cgaattcact cacaaagagg     660
cgacgcgccc cttgacaaag tcgccgacga tgccaacacc cgttggtacg caacacatgc     720
tgcaccagac gtgcaccccg aagcgaagtt cgacaccgtc aacaggaagc aaaagcagca     780
gtcgaccgct tcgccccagc aacaccagaa atatcgacga gccccctatg actacgccag     840
caaggacaag gcccagaacc gatatgcgca gcaccctatc cgcgaatccg agaaaccaaa     900
ctacgtaaaa gtccccaacg atgcgagcgc cctcgcaact ttagctccgg ctcagcccgt     960
ccgagcacca cacacctcac gacatcactg gcccagcagc agcgccgctt ctgggctggc    1020
ctcgccgcac aatgcgcgga gtctggagga ctgggaagtt gaagactttg ttcttctggc    1080
gaccgtcgat ggagacctct atgccagcga ccgaaagacc ggtcggcacc tctggcacct    1140
cgaggtcgac cagccagtgg ttgaaaccaa acactaccga acaaacaact ccgtcctcga    1200
cgacgactat cgccccgtcg accactacat ctgggccgtc gagccgagcc gcgatggagg    1260
gctctatgta tggatccccg actccggagc gggcctcgtc aggaccggct tcaccatgaa    1320
```

11

```
gcacctcgtt gaagaacttg ctccatacgc cggcgacgag cccccgttg tctataccgg      1380
agacaagaag acgaccatgg tcaccctgga cgccgctacc gggcgcgttc tcaaatggtt      1440
tggctctagc ggctcccaag tcaacgaagc cgagagctgc cttcggccca atgcctttga      1500
cgacagggat accacagagt gcagctccat gggcacaatc acgctgggaa ggaccgagta      1560
cacggtgggc atccagaggc gagacggtcg ccctatcgca accttgaagt acgcagaatg      1620
gggacccaac acctttgaca gcgacctcta ccagcaatac cacgcctcgt tggacaacca      1680
ttacatcacc agtcagcacg acgggagaat ttacgcgttt gacaagtcac aggcagaaaa      1740
cgacctgccc ctctacaccc caagtttttc gtctcccgtc gcccgggtct tcgatgtctg      1800
tcgaccgtgg gatgcgaatg cgggaagcaa cccggagctg gtggttctcc cccaacctcc      1860
aattccagcg cttgatgaga gcactgtcaa gatgcgaagc aacagcatct tcctcaacca      1920
gactgaaagc ggcgactggt atgcgctctc cggccgtgcg tatccgctta tactcgatgc      1980
ccccgtggcc cagatctcgc gggacgactt gtgggatatg cccatgcct ttgattccat       2040
taacccaaat aagctgtcca aggccctggt gggaacccac tttctgaatc ccgtcaagag      2100
caccggttac catcagccgc cgacgctccc tgccggcgcc ctcgacgagt attacgagga      2160
cttggagaac gcctcaaaca atgctcacgc cgtgacaaac actgttccgg aggagcccac      2220
catcatcacc aaagtcaagg ctcttccgca gagtgctgcg aacagcgtca ttgactttgt      2280
cagcaacccc attctcatca ttttcttgat aggctccttg atctacaacg aaaagaagct      2340
gcgacggtcg tatcatcggt tccggactca tggcacaatc aaggacgtct atcccttctt      2400
cgttatcgaa tctgaggccg gagatgaatc aggtgatgac aaggacggtg tgttcccatc      2460
ttcgccgtct ccgcgcagtc aaccccagga ccaaaatgcg gaagaccacc tgtccagaca      2520
caaggtggag aggaatgccg gcgaccagga caaggtcaag acaacagga gcctgcatga       2580
cgtttctgac accttggaac cgagcaacaa gactgttgag aaaacggccg atgtggtcaa      2640
gcaagtggat gtagctggcc ctgacgcacc ctcgacggac tccaatggtg ctgcaccgga      2700
gaagaagaag aaggctcacc gaggccgtcg tggcggtgtc aagcacagaa agggtcggcc      2760
caccgacggc tcgcagtctc atgaaaacga cccagctctc actacagtgg acgaggctgt      2820
aagcaatgcg aagaagctgg gtgaccggcc aagcctggaa cccgacgtca tgaccatcta      2880
caacgacatg caagccgtca cgggctctgt tatcagcatg ggaaacatcg aggtcgatac      2940
ggatgtcgag cttggcatgg gcagcaacgg tactgtcgta tttgctggcc gattcgatgg      3000
cagggacgtc gccgtcaaga gaatgacgat tcagttctac gacattgcca cgcgagaaac      3060
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gcgaggcgac ttcctgtata ttgccttgga acgctgcgct gcttcattgg cagatgtcat      3240
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cttgtaccaa atcaccaacg gcatcagcca cttgcactct ctgcggattg ttcatcgaga      3360
cttgaagcct caaaacatct tggtcaactt ggacaaggac ggcagaccaa ggctcttggt      3420
gtcggacttt ggcctgtgta agaaactgga ggatagacag tcttcgttcg gagcaacgac      3480
aggccgagcc gctggaacgt cgggatggcg tgcccccgaa ctgcttctcg atgacgacgg      3540
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agaccccaac tcgctttcca atggagggcg agccacgagg gccattgaca tcttctccct      3660
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gcctgccttg gtcgagctgg agcgacatgc gccggaggtc attaagggag acttcttgaa      4020
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aagaaaggcc tcttgcttgt ttggttgctg tatatctttt gctcgaaga tggaaacgga       4380
aaatattggg gaagttgcat gggaagtgaa caaaagaggg gaaaaatggt gaatgtgaaa      4440
gcaaagtcgg ttagcgggtg gcatggtcg tcatccatgt aattgtttca gcttctgttg       4500
catcaaaagc gttgtgtttt cgttctttt                                        4528
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<210> 14
<211> 1232

12

<212> PRT
<213> Trichoderma reesei

<400> 14
Met Val Arg Val Ala Ser Glu Ala Leu Leu Ala Phe Ala Phe Ile Leu
1   5   10   15
Ile Pro Trp Leu Gln Leu Ala Asp Ala Gln Gln Gln Pro Gln Gln Pro
            20   25   30
Gln Ile Arg Ile His Ser Gln Arg Gly Asp Ala Pro Leu Asp Lys Val
        35   40   45
Ala Asp Asp Ala Asn Thr Arg Trp Tyr Ala Thr His Ala Ala Pro Asp
    50   55   60
Val His Pro Glu Ala Lys Phe Asp Thr Val Asn Arg Lys Gln Lys Gln
65   70   75   80
Gln Ser Thr Ala Ser Pro Gln Gln His Gln Lys Tyr Arg Arg Ala Pro
                85   90   95
Tyr Asp Tyr Ala Ser Lys Asp Lys Ala Gln Asn Arg Tyr Ala Gln His
            100   105   110
Pro Ile Arg Glu Ser Glu Lys Pro Asn Tyr Val Lys Val Pro Asn Asp
        115   120   125
Ala Ser Ala Leu Ala Thr Leu Ala Pro Ala Gln Pro Val Arg Ala Pro
    130   135   140
His Thr Ser Arg His His Trp Pro Ser Ser Ser Ala Ala Ser Gly Leu
145   150   155   160
Ala Ser Pro His Asn Ala Arg Ser Leu Glu Asp Trp Glu Val Glu Asp
                165   170   175
Phe Val Leu Leu Ala Thr Val Asp Gly Asp Leu Tyr Ala Ser Asp Arg
            180   185   190
Lys Thr Gly Arg His Leu Trp His Leu Glu Val Asp Gln Pro Val Val
        195   200   205
Glu Thr Lys His Tyr Arg Thr Asn Asn Ser Val Leu Asp Asp Asp Tyr
    210   215   220
Arg Pro Val Asp His Tyr Ile Trp Ala Val Glu Pro Ser Arg Asp Gly
225   230   235   240
Gly Leu Tyr Val Trp Ile Pro Asp Ser Gly Ala Gly Leu Val Arg Thr
            245   250   255
Gly Phe Thr Met Lys His Leu Val Glu Glu Leu Ala Pro Tyr Ala Gly
        260   265   270
Asp Glu Pro Pro Val Val Tyr Thr Gly Asp Lys Lys Thr Thr Met Val
        275   280   285
Thr Leu Asp Ala Ala Thr Gly Arg Val Leu Lys Trp Phe Gly Ser Ser
    290   295   300
Gly Ser Gln Val Asn Glu Ala Glu Ser Cys Leu Arg Pro Asn Ala Phe
305   310   315   320
Asp Asp Arg Asp Thr Thr Glu Cys Ser Ser Met Gly Thr Ile Thr Leu
            325   330   335
Gly Arg Thr Glu Tyr Thr Val Gly Ile Gln Arg Arg Asp Gly Arg Pro
        340   345   350
Ile Ala Thr Leu Lys Tyr Ala Glu Trp Gly Pro Asn Thr Phe Asp Ser
    355   360   365
Asp Leu Tyr Gln Gln Tyr His Ala Ser Leu Asp Asn His Tyr Ile Thr
    370   375   380
Ser Gln His Asp Gly Arg Ile Tyr Ala Phe Asp Lys Ser Gln Ala Glu
385   390   395   400
Asn Asp Leu Pro Leu Tyr Thr His Lys Phe Ser Ser Pro Val Ala Arg
            405   410   415
Val Phe Asp Val Cys Arg Pro Trp Asp Ala Asn Ala Gly Ser Asn Pro

13

```
                  420                    425                    430
Glu Leu Val Val Leu Pro Gln Pro Pro Ile Pro Ala Leu Asp Glu Ser
          435                    440                    445
Thr Val Lys Met Arg Ser Asn Ser Ile Phe Leu Asn Gln Thr Glu Ser
          450                    455                    460
Gly Asp Trp Tyr Ala Leu Ser Gly Arg Ala Tyr Pro Leu Ile Leu Asp
465                    470                    475                    480
Ala Pro Val Ala Gln Ile Ser Arg Asp Asp Leu Trp Asp Met Ala His
              485                    490                    495
Ala Phe Asp Ser Ile Asn Pro Asn Lys Leu Ser Lys Ala Leu Val Gly
          500                    505                    510
Thr His Phe Leu Asn Pro Val Lys Ser Thr Gly Tyr His Gln Pro Pro
          515                    520                    525
Thr Leu Pro Ala Gly Ala Leu Asp Glu Tyr Tyr Glu Asp Leu Glu Asn
          530                    535         ·          540
Ala Ser Asn Asn Ala His Ala Val Thr Asn Thr Val Pro Glu Glu Pro
545                    550                    555                    560
Thr Ile Ile Thr Lys Val Lys Ala Leu Pro Gln Ser Ala Ala Asn Ser
              565                    570                    575
Val Ile Asp Phe Val Ser Asn Pro Ile Leu Ile Ile Phe Leu Ile Gly
          580                    585                    590
Ser Leu Ile Tyr Asn Glu Lys Lys Leu Arg Arg Ser Tyr His Arg Phe
          595                    600                    605
Arg Thr His Gly Thr Ile Lys Asp Val Tyr Pro Phe Phe Val Ile Glu
          610                    615                    620
Ser Glu Ala Gly Asp Glu Ser Gly Asp Asp Lys Asp Gly Val Phe Pro
625                    630                    635                    640
Ser Ser Pro Ser Pro Arg Ser Gln Pro Gln Asp Gln Asn Ala Glu Asp
              645                    650                    655
His Leu Ser Arg His Lys Val Glu Arg Asn Ala Gly Asp Gln Asp Lys
          660                    665                    670
Val Lys Asp Asn Arg Ser Leu His Asp Val Ser Asp Thr Leu Glu Pro
          675                    680                    685
Ser Asn Lys Thr Val Glu Lys Thr Ala Asp Val Val Lys Gln Val Asp
          690                    695                    700
Val Ala Gly Pro Asp Ala Pro Ser Thr Asp Ser Asn Gly Ala Ala Pro
705                    710                    715                    720
Glu Lys Lys Lys Lys Ala His Arg Gly Arg Arg Gly Gly Val Lys His
              725                    730                    735
Arg Lys Gly Arg Pro Thr Asp Gly Ser Gln Ser His Glu Asn Asp Pro
          740                    745                    750
Ala Leu Thr Thr Val Asp Glu Ala Val ·Ser Asn Ala Lys Lys Leu Gly
          755                    760                    765
Asp Arg Pro Ser Leu Glu Pro Asp Val Met Thr Ile Tyr Asn Asp Met
          770                    775                    780
Gln Ala Val Thr Gly Ser Val Ile Ser Met Gly Asn Ile Glu Val Asp
785                    790                    795                    800
Thr Asp Val Glu Leu Gly Met Gly Ser Asn Gly Thr Val Val Phe Ala
              805                    810                    815
Gly Arg Phe Asp Gly Arg Asp Val Ala Val Lys Arg Met Thr Ile Gln
          820                    825                    830
Phe Tyr Asp Ile Ala Thr Arg Glu Thr Lys Leu Leu Arg Glu Ser Asp
          835                    840                    845
Asp His Pro Asn Val Ile Arg Tyr Tyr Ser Gln Val Gln Arg Gly Asp
          850                    855                    860
Phe Leu Tyr Ile Ala Leu Glu Arg Cys Ala Ala Ser Leu Ala Asp Val
865                    870                    875                    880
```

14

```
Ile Glu Lys Pro Tyr Ala Phe Gly Glu Leu Ala Lys Ala Gly Gln Lys
              885             890             895
Asp Leu Pro Gly Val Leu Tyr Gln Ile Thr Asn Gly Ile Ser His Leu
              900             905             910
His Ser Leu Arg Ile Val His Arg Asp Leu Lys Pro Gln Asn Ile Leu
          915             920             925
Val Asn Leu Asp Lys Asp Gly Arg Pro Arg Leu Leu Val Ser Asp Phe
      930             935             940
Gly Leu Cys Lys Lys Leu Glu Asp Arg Gln Ser Ser Phe Gly Ala Thr
  945             950             955             960
Thr Gly Arg Ala Ala Gly Thr Ser Gly Trp Arg Ala Pro Glu Leu Leu
              965             970             975
Leu Asp Asp Asp Gly Gln Asn Pro Ala Ala Ile Asp Ser Ser Thr His
              980             985             990
Ser Gly Ser His Thr Ile Leu Val Gly Asp Pro Asn Ser Leu Ser Asn
          995             1000            1005
Gly Gly Arg Ala Thr Arg Ala Ile Asp Ile Phe Ser Leu Gly Leu Val
      1010            1015            1020
Phe Phe Tyr Val Leu Thr Asn Gly Ser His Pro Phe Asp Cys Gly Asp
  1025            1030            1035            1040
Arg Tyr Met Arg Glu Val Asn Ile Arg Lys Gly Asn Tyr Asn Leu Asp
              1045            1050            1055
Pro Leu Asp Ala Leu Gly Asp Phe Ala Tyr Glu Ala Lys Asp Leu Ile
          1060            1065            1070
Ala Ser Met Leu Gln Ala Ser Pro Lys Ala Arg Pro Asp Ser Arg Glu
          1075            1080            1085
Val Met Ala His Pro Phe Phe Trp Ser Pro Lys Lys Arg Leu Ala Phe
   1090            1095            1100
Leu Cys Asp Val Ser Asp Ser Leu Glu Lys Glu Val Arg Asp Pro Pro
1105            1110            1115            1120
Pro Ala Leu Val Glu Leu Glu Arg His Ala Pro Glu Val Ile Lys Gly
              1125            1130            1135
Asp Phe Leu Lys Val Leu Thr Arg Asp Phe Val Glu Ser Leu Gly Lys
          1140            1145            1150
Gln Arg Lys Tyr Thr Gly Asn Lys Leu Leu Asp Leu Leu Arg Ala Leu
          1155            1160            1165
Arg Asn Lys Arg Asn His Tyr Glu Asp Met Ser Asp Ser Leu Lys Arg
      1170            1175            1180
Ser Val Gly Ser Leu Pro Asp Gly Tyr Leu Ala Tyr Trp Thr Val Lys
1185            1190            1195            1200
Phe Pro Met Leu Leu Leu Thr Cys Trp Asn Val Val Tyr Asn Leu Glu
          1205            1210            1215
Trp Glu Lys Thr Asp Arg Phe Arg Glu Tyr Tyr Glu Pro Ala Gly Leu
          1220            1225            1230
```

<210> 15
<211> 1669
<212> DNA
<213> Aspergillus niger

<400> 15
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cttttattg ttctatggtt cttaaggaca cctgtccttc ttggccctat ccttcttgtt        60
gtctggtaca cttgacccca ggcaccactt ggccaggcct ggcccccca gcttcccccg       120
ttatgacacg gtggcctgtg ttcctgtgac acgggcaagc agacgtcctc cacaagctgt       180
gtcgacctac atcaccgtcc tcccttgcag tgcggttaag ataaggctca tagtaaatcg       240
attgatccac aattaaagat caatcacctg tcacgcttga aatgatggaa gaagcattct       300
ctccagtcga ctccctcgcc ggctccccga cgcctgagtt gccattgttg acagtgtccc       360
```

```
cggcggacac gtcgcttgat gactcgtcag tacaggcagg ggagaccaag gcggaagaga        420
agaagcctgt gaagaagaga aagtcatggg gccaggaatt gccagtcccg aagactaact        480
tgccccaag gaaacgggcc aagactgaag atgagaaaga gcaacgtcgt atcgagcgcg         540
ttcttcgcaa tcgtgcggca gcacaaacat cacgcgagcg caagaggctc gaaatggaga        600
agttggaaaa tgagaagatt cagatggaac agcaaaacca gttccttctg caacgactat        660
cccagatgga agctgagaac aatcgcttaa accaacaagt cgctcaacta tctgctgagg        720
tccggggctc ccgtggcaac actcccaagc ccggctcccc cgtctcagct tctcctaccc        780
taactcctac cctatttaaa caagaacgcg acgaaatccc tcttgaacgg attcctttcc        840
ccacaccctc tatcaccgac tactcccta ccttgaggcc ttccactctg ctgagtcct         900
ccgacgtgac acaacatcct gcagcggtgt tgtgcgacct gcagtgtccg tcgctggact        960
cgaaggagaa ggaagtgccc tctctctctt tgacgtcggc tcaaaccctg aacctcacgc       1020
tgccgatgat cttgcagctc ctctttctga cgatgacttc caccgcctat tcaacgttga       1080
ttcacccgtt gggtcagatt cttcagtcct tgaagacggg ttcgcctttg acgttctcga       1140
cggaggagat ctatcagcat ttccatttga ttctatggtt gatttcgacc ccgaatctgt       1200
tggcttcgaa ggcatcgagc cgcccccacgg tcttccggat gagacttctc gccagacttc      1260
tagcgtgcaa cccagccttg cgcgtccac ttcgcgatgc gacgggcagg gcattgcagc        1320
tggctgttag cgagcagttt cgccaggag atgcatcggc tgtcgatggt aacggagtcc        1380
aatggagctg ggagtctttg ttgaccttgg cgtggacgat agacctactc gaacagccgg       1440
gacgacgcaa acgaatcttg agcggtttga aatcagcgaa aactggacgg cgaagtaata       1500
ttggcaagtc tcaaaggagt acacggagtt catggagttc acgaagcacc caagaggcgt       1560
tgacgtctct ccttatgggc aagcatagtt gaggttccgg ctgtaaatta tcataaatcc       1620
ttataatttt attctagatt tcaatacagc agttgattgt ctgctcatc                   1669
```

<210> 16
<211> 386
<212> PRT
<213> Aspergillus niger

<400> 16

```
Met Val Leu Lys Asp Thr Cys Pro Ser Trp Pro Tyr Pro Ser Cys Cys
  1           5               10               15
Leu Val His Leu Thr Pro Gly Thr Thr Trp Pro Gly Leu Ala Pro Pro
          20               25               30
Ala Ser Pro Val Met Thr Arg Trp Pro Val Phe Leu Met Met Glu Glu
          35               40               45
Ala Phe Ser Pro Val Asp Ser Leu Ala Gly Ser Pro Thr Pro Glu Leu
      50               55               60
Pro Leu Leu Thr Val Ser Pro Ala Asp Thr Ser Leu Asp Asp Ser Ser
 65               70               75               80
Val Gln Ala Gly Glu Thr Lys Ala Glu Glu Lys Lys Pro Val Lys Lys
              85               90               95
Arg Lys Ser Trp Gly Gln Glu Leu Pro Val Pro Lys Thr Asn Leu Pro
          100              105              110
Pro Arg Lys Arg Ala Lys Thr Glu Asp Glu Lys Glu Gln Arg Arg Ile
          115              120              125
Glu Arg Val Leu Arg Asn Arg Ala Ala Ala Gln Thr Ser Arg Glu Arg
      130              135              140
Lys Arg Leu Glu Met Glu Lys Leu Glu Asn Glu Lys Ile Gln Met Glu
145              150              155              160
Gln Gln Asn Gln Phe Leu Leu Gln Arg Leu Ser Gln Met Glu Ala Glu
              165              170              175
Asn Asn Arg Leu Asn Gln Gln Val Ala Gln Leu Ser Ala Glu Val Arg
          180              185              190
Gly Ser Arg Gly Asn Thr Pro Lys Pro Gly Ser Pro Val Ser Ala Ser
          195              200              205
Pro Thr Leu Thr Pro Thr Leu Phe Lys Gln Glu Arg Asp Glu Ile Pro
      210              215              220
```

16

```
Leu Glu Arg Ile Pro Phe Pro Thr Pro Ser Ile Thr Asp Tyr Ser Pro
225             230             235             240
Thr Leu Arg Pro Ser Thr Leu Ala Glu Ser Ser Asp Val Thr Gln His
            245             250             255
Pro Ala Val Ser Val Ala Gly Leu Glu Gly Glu Gly Ser Ala Leu Ser
            260             265             270
Leu Phe Asp Val Gly Ser Asn Pro Glu Pro His Ala Ala Asp Asp Leu
        275             280             285
Ala Ala Pro Leu Ser Asp Asp Asp Phe His Arg Leu Phe Asn Val Asp
        290             295             300
Ser Pro Val Gly Ser Asp Ser Ser Val Leu Glu Asp Gly Phe Ala Phe
305             310             315             320
Asp Val Leu Asp Gly Gly Asp Leu Ser Ala Phe Pro Phe Asp Ser Met
            325             330             335
Val Asp Phe Asp Pro Glu Ser Val Gly Phe Glu Gly Ile Glu Pro Pro
        340             345             350
His Gly Leu Pro Asp Glu Thr Ser Arg Gln Thr Ser Ser Val Gln Pro
        355             360             365
Ser Leu Gly Ala Ser Thr Ser Arg Cys Asp Gly Gln Gly Ile Ala Ala
        370             375             380
Gly Cys
385


<210> 17
<211> 20
<212> DNA
<213> Aspergillus niger


<400> 17
cggtgttgtg cgacctgcag                                                    20


<210> 18
<211> 44
<212> PRT
<213> Aspergillus niger


<400> 18
Met Val Leu Lys Asp Thr Cys Pro Ser Trp Pro Tyr Pro Ser Cys Cys
1               5               10              15
Leu Val His Leu Thr Pro Gly Thr Thr Trp Pro Gly Leu Ala Pro Pro
            20              25              30
Ala Ser Pro Val Met Thr Arg Trp Pro Val Phe Leu
        35              40


<210> 19
<211> 342
<212> PRT
<213> Aspergillus niger


<400> 19
Met Met Glu Glu Ala Phe Ser Pro Val Asp Ser Leu Ala Gly Ser Pro
1               5               10              15
Thr Pro Glu Leu Pro Leu Leu Thr Val Ser Pro Ala Asp Thr Ser Leu
            20              25              30
Asp Asp Ser Ser Val Gln Ala Gly Glu Thr Lys Ala Glu Glu Lys Lys
        35              40              45
Pro Val Lys Lys Arg Lys Ser Trp Gly Gln Glu Leu Pro Val Pro Lys
```

17

```
                50                        55                        60
Thr Asn Leu Pro Pro Arg Lys Arg Ala Lys Thr Glu Asp Glu Lys Glu
65                        70                        75                        80
Gln Arg Arg Ile Glu Arg Val Leu Arg Asn Arg Ala Ala Ala Gln Thr
                    85                        90                        95
Ser Arg Glu Arg Lys Arg Leu Glu Met Glu Lys Leu Glu Asn Glu Lys
                100                        105                        110
Ile Gln Met Glu Gln Gln Asn Gln Phe Leu Leu Gln Arg Leu Ser Gln
            115                        120                        125
Met Glu Ala Glu Asn Asn Arg Leu Asn Gln Gln Val Ala Gln Leu Ser
            130                        135                        140
Ala Glu Val Arg Gly Ser Arg Gly Asn Thr Pro Lys Pro Gly Ser Pro
145                        150                        155                        160
Val Ser Ala Ser Pro Thr Leu Thr Pro Thr Leu Phe Lys Gln Glu Arg
                165                        170                        175
Asp Glu Ile Pro Leu Glu Arg Ile Pro Phe Pro Thr Pro Ser Ile Thr
            180                        185                        190
Asp Tyr Ser Pro Thr Leu Arg Pro Ser Thr Leu Ala Glu Ser Ser Asp
            195                        200                        205
Val Thr Gln His Pro Ala Val Ser Val Ala Gly Leu Glu Gly Glu Gly
            210                        215                        220
Ser Ala Leu Ser Leu Phe Asp Val Gly Ser Asn Pro Glu Pro His Ala
225                        230                        235                        240
Ala Asp Asp Leu Ala Ala Pro Leu Ser Asp Asp Asp Phe His Arg Leu
                245                        250                        255
Phe Asn Val Asp Ser Pro Val Gly Ser Asp Ser Ser Val Leu Glu Asp
            260                        265                        270
Gly Phe Ala Phe Asp Val Leu Asp Gly Gly Asp Leu Ser Ala Phe Pro
            275                        280                        285
Phe Asp Ser Met Val Asp Phe Asp Pro Glu Ser Val Gly Phe Glu Gly
            290                        295                        300
Ile Glu Pro Pro His Gly Leu Pro Asp Glu Thr Ser Arg Gln Thr Ser
305                        310                        315                        320
Ser Val Gln Pro Ser Leu Gly Ala Ser Thr Ser Arg Cys Asp Gly Gln
                325                        330                        335
Gly Ile Ala Ala Gly Cys
                340
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<210> 20
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 20
atcgcaggat tcccacctac gacaacaacc gccact   36

<210> 21
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

.18

<400> 21
tacagcggat ccctatggat tacgccaatt gtcaag   36

<210> 22
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 22
ccacctacga caacaaccgc cactatggaa atgactgatt ttgaactact tgcctcgtcc   60
ccgccgggtc ac   72

<210> 23
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 23
aattataccc tcttgcgatt gtcttcatga agtgatgaag aaatcattga cactggatgg   60
cggcgttagt atcga   75

<210> 24
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 24
gccatccttg gtgactgagc c   21

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 25
caattgctcg ctcttacatt gaat   24

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

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<400> 26
aattaaccct cactaaaggg                                              20


<210> 27
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 27
tggttgatga cgacgatgcg aacagtcatg acaggcaacg                        40


<210> 28
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> HAC1-specific oligonucleotide

<400> 28
gggagacgac tgctggaacg ccat                                         24


<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 29
ccccgagcag tccttgatgg                                              20


<210> 30
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 30
gtcgttgatg tcgaagt                                                 17


<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 31
gtaatacgac tcactatagg gc                                           22
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20

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<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 32
ttaggacaga ggccacggtg t                                              21

<210> 33
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 33
cccatccttg gtgactgagc c                                        .     21

<210> 34
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 34
aagagtcggt gtcagagttg g                                              21

<210> 35
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 35
attaatattt tagcactttg aaaaatgcgt ctacttcgaa gaaacatgct tgcctcgtcc    60
ccgccgggtc ac                                                        72

<210> 36
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 36
aagcagaggg gcatgaacat gttatgaata caaaaattca cgtaaaatgt cgacactgga    60
tggcggcgtt agtat                                                     75
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21

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 37
ccgcaacacg acacggcagg caac   24

<210> 38
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 38
ctaggtagac gttgtatttt g   21

<210> 39
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 39
tcgaacggat ccgaaaagaa gcccgtcaag aagagg   36

<210> 40
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 40
atcgcaggat ccctaggttt ggccatcccg cgagccaaa   39

<210> 41
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 41
cggctgaacc agcgcggcag ccagatgtgg ccaaaggg   38

<210> 42

22

<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 42
ggtacctgct aaccagcgcg gcatgattca ac   32

<210> 43
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 43
ggatcttgca tagccagatg tggcctcgat tgact   35

<210> 44
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 44
ggattagaaa acgccaacgt gtccataacg gtc   33

<210> 45
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 45
gggcgtggag aagcgagaag tggcctcttc ttctcc   36

<210> 46
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> binding consensus sequence

<221> misc_feature
<222> (1)...(11)
<223> n = AW or C

<400> 46
gcsarngtgk c   11

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<210> 47
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 47
gtggtaatat tacctttaca g                                              21

<210> 48
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 48
caatttcaat acgggtggac                                                20

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 49
tgtcatcact gctccatctt                                                20

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 50
ttaagccttg gcaacatatt                                                20

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 51
ttgaacagca gatcgttact g                                              21

<210> 52
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<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 52
tataaagttc gtcaatagtg g   21

<210> 53
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 53
cggaggcaag agtcatagac g   21

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 54
caatatattt ctgaaccagt acg   23

<210> 55
<211> 45
<212> RNA
<213> Trichoderma reesei

<400> 55
acugauucga cacaacgucc ugcagagaug uugugcgacc cgcag   45

<210> 56
<211> 45
<212> RNA
<213> Aspergillus nidulans

<400> 56
cccgauuuga cacaacaucc ugcagcgaug uugugcgacc ugcag   45

<210> 57
<211> 28
<212> RNA
<213> Saccharomyces cerevisiae

<400> 57
ccuuguacug uccgaagcgc agucaggu   28

<210> 58

<211> 60
<212> DNA
<213> Trichoderma reesei

<400> 58
ccactgattc gacacaacgt cctgcagaga tgttgtgcga cccgcagtgt caatcggtgg   60

<210> 59
<211> 60
<212> DNA
<213> Aspergillus nidulans

<400> 59
cccccgattt gacacaacat cctgcagcga tgttgtgcga cctgcagtgt cagtcggcgg   60

<210> 60
<211> 68
<212> PRT
<213> Saccharomyces cerevisiae

<400> 60
Lys Ser Thr Leu Pro Pro Arg Lys Arg Ala Lys Thr Lys Glu Glu Lys
1   5   10   15
Glu Gln Arg Arg Ile Glu Arg Ile Leu Arg Asn Arg Arg Ala Ala His
            20   25   30
Gln Ser Arg Glu Lys Lys Arg Leu His Leu Gln Tyr Leu Glu Arg Lys
        35   40   45
Cys Ser Leu Leu Glu Asn Leu Leu Asn Ser Val Asn Leu Glu Lys Leu
    50   55   60
Ala Asp His Glu
65

<210> 61
<211> 12
<212> DNA
<213> Trichoderma reesei

<400> 61
gccagatgtg gc   12

<210> 62
<211> 11
<212> DNA
<213> Trichoderma reesei

<400> 62
gccaacgtgt c   11

<210> 63
<211> 12
<212> DNA
<213> Trichoderma reesei

<400> 63
gcgagaagtg gc   12